



SEQUENCE LISTING

<110> KNUTZON, DEBORAH
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<120> METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN
POLYUNSATURATED FATTY ACIDS

<130> CGAB-210 USA

<140> 09/367,013

<141> 1999-08-05

<150> 08/834,655

<151> 1997-04-11

<160> 40

<170> PatentIn Ver. 2.1

<210> 1

<211> 1617

<212> DNA

<213> Mortierella alpina

<220>

<223> Description of Combined DNA/RNA Molecule:

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<210> 2

<211> 457

<212> PRT

<213> Mortierella alpina

<400> 2

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Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
35 40 45

Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
50 55 60

Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
65 70 75 80

Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
85 90 95

Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
100 105 110

Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
115 120 125

Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
130 135 140

Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu

145		150		155		160
Gly Leu Phe Trp	Gln Gln Cys Gly Trp	Leu Ala His Asp	Phe Leu His			
	165	170	175			
His Gln Val Phe	Gln Asp Arg Phe Trp	Gly Asp Leu Phe	Gly Ala Phe			
	180	185	190			
Leu Gly Gly Val	Cys Gln Gly Phe Ser	Ser Ser Trp Trp	Lys Asp Lys			
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His Asn Thr His	His Ala Ala Pro Asn	Val His Gly Glu	Asp Pro Asp			
	210	215	220			
Ile Asp Thr His	Pro Leu Leu Thr Trp	Ser Glu His Ala	Leu Glu Met			
	225	230	235	240		
Phe Ser Asp Val	Pro Asp Glu Glu Leu	Thr Arg Met Trp	Ser Arg Phe			
	245	250	255			
Met Val Leu Asn	Gln Thr Trp Phe Tyr	Phe Pro Ile Leu	Ser Phe Ala			
	260	265	270			
Arg Leu Ser Trp	Cys Leu Gln Ser Ile	Leu Phe Val Leu	Pro Asn Gly			
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Gln Ala His Lys	Pro Ser Gly Ala Arg	Val Pro Ile Ser	Leu Val Glu			
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Gln Leu Ser Leu	Ala Met His Trp Thr	Trp Tyr Leu Ala	Thr Met Phe			
	305	310	315	320		
Leu Phe Ile Lys	Asp Pro Val Asn Met	Leu Val Tyr Phe	Leu Val Ser			
	325	330	335			
Gln Ala Val Cys	Gly Asn Leu Leu Ala	Ile Val Phe Ser	Leu Asn His			
	340	345	350			
Asn Gly Met Pro	Val Ile Ser Lys Glu	Glu Ala Val Asp	Met Asp Phe			
	355	360	365			
Phe Thr Lys Gln	Ile Ile Thr Gly Arg	Asp Val His Pro	Gly Leu Phe			
	370	375	380			
Ala Asn Trp Phe	Thr Gly Gly Leu Asn	Tyr Gln Ile Glu	His His Leu			
	385	390	395	400		
Phe Pro Ser Met	Pro Arg His Asn Phe	Ser Lys Ile Gln	Pro Ala Val			

405

410

415

Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
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Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
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Ala Ala Ser Lys Met Gly Lys Ala Gln
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<210> 3

<211> 1488

<212> DNA

<213> Mortierella alpina

<400> 3

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<210> 4

<211> 399

<212> PRT

<213> Mortierella alpina

<400> 4

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Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
35 40 45

His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
50 55 60

Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
65 70 75 80

Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
85 90 95

Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
100 105 110

Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
115 120 125

Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
130 135 140

Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp
145 150 155 160

Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
165 170 175

Glu Asn Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
180 185 190

Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
195 200 205

Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
210 215 220

Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
225 230 235 240

Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
245 250 255

Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
260 265 270

Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
275 280 285

Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
290 295 300

Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
305 310 315 320

Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
325 330 335

Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
340 345 350

Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
355 360 365

Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
370 375 380

Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
385 390 395

<210> 5

<211> 355

<212> PRT

<213> Mortierella alpina

<400> 5

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20 25 30

Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
35 40 45

Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
50 55 60

Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
 65 70 75 80

Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
 85 90 95

Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
 100 105 110

Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
 115 120 125

Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
 130 135 140

Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
 145 150 155 160

Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
 165 170 175

Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser
 180 185 190

Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
 195 200 205

His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
 210 215 220

Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
 225 230 235 240

Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
 245 250 255

Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
 260 265 270

Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
 275 280 285

Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
 290 295 300

His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
 305 310 315 320

Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu
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Val Phe Ser Arg Leu Asn Glu Val Ser Lys Ala Ala Ser Lys Met Gly
 340 345 350

Lys Ala Gln
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<210> 6

<211> 104

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> Amino acids 27, 48 and 63 uncertain of sequence

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 20 25 30

Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
 35 40 45

Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
 50 55 60

Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp
 65 70 75 80

Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr
 85 90 95

Gly Pro Asn Leu Gln His Ile Pro
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<210> 7

<211> 252

<212> PRT

<213> Arabidopsis thaliana

<400> 7

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Gly	His	Asp	Ser	Gly	His	Tyr	Val	Ile	Met	Ser	Asn	Lys	Ser	Tyr	Asn	35	40	45	
Arg	Phe	Ala	Gln	Leu	Leu	Ser	Gly	Asn	Cys	Leu	Thr	Gly	Ile	Ser	Ile	50	55	60	
Ala	Trp	Trp	Lys	Trp	Thr	His	Asn	Ala	His	His	Leu	Ala	Cys	Asn	Ser	65	70	75	80
Leu	Asp	Tyr	Asp	Pro	Asp	Leu	Gln	His	Ile	Pro	Val	Phe	Ala	Val	Ser	85	90	95	
Thr	Lys	Phe	Phe	Ser	Ser	Leu	Thr	Ser	Arg	Phe	Tyr	Asp	Arg	Lys	Leu	100	105	110	
Thr	Phe	Gly	Pro	Val	Ala	Arg	Phe	Leu	Val	Ser	Tyr	Gln	His	Phe	Thr	115	120	125	
Tyr	Tyr	Pro	Val	Asn	Cys	Phe	Gly	Arg	Ile	Asn	Leu	Phe	Ile	Gln	Thr	130	135	140	
Phe	Leu	Leu	Leu	Phe	Ser	Lys	Arg	Glu	Val	Pro	Asp	Arg	Ala	Leu	Asn	145	150	155	160
Phe	Ala	Gly	Ile	Leu	Val	Phe	Trp	Thr	Trp	Phe	Pro	Leu	Leu	Val	Ser	165	170	175	
Cys	Leu	Pro	Asn	Trp	Pro	Glu	Arg	Phe	Phe	Phe	Val	Phe	Thr	Ser	Phe	180	185	190	
Thr	Val	Thr	Ala	Leu	Gln	His	Ile	Gln	Phe	Thr	Leu	Asn	His	Phe	Ala	195	200	205	
Ala	Asp	Val	Tyr	Val	Gly	Pro	Pro	Thr	Gly	Ser	Asp	Trp	Phe	Glu	Lys	210	215	220	
Gln	Ala	Ala	Gly	Thr	Ile	Asp	Ile	Ser	Cys	Arg	Ser	Tyr	Met	Asp	Trp	225	230	235	240
Phe	Phe	Gly	Gly	Leu	Gln	Phe	Gln	Leu	Glu	His	His	245	250						

<210> 8

<211> 125

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> Amino acids 2, 3, 30, 121 and 125 uncertain of
sequence

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Leu Leu Val Ser Cys Leu Pro Asn Trp Pro Glu Arg Phe Xaa Phe Val
20 25 30

Phe Thr Gly Phe Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu
35 40 45

Asn His Phe Ala Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp
50 55 60

Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
65 70 75 80

Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
85 90 95

Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
100 105 110

Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
115 120 125

<210> 9

<211> 131

<212> PRT

<213> Homo sapiens

<400> 9

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1 5 10 15

Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
20 25 30

Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
 35 40 45

Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
 50 55 60

Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
 65 70 75 80

Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
 85 90 95

His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
 100 105 110

Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
 115 120 125

Lys Pro Leu
 130

<210> 10

<211> 87

<212> PRT

<213> Caenorhabditis elegans

<400> 10

Cys Ser Pro Lys Ser Ser Pro Thr Arg Asn Met Thr Pro Ser Pro Phe
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Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 20 25 30

Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val
 35 40 45

Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
 50 55 60

Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu
 65 70 75 80

Leu Val Gln Ala Lys Ala Ala
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<210> 11

<211> 143
<212> PRT
<213> Homo sapiens

<220>

<223> Amino acid 125 uncertain of sequence

<400> 11

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20 25 30

Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu
35 40 45

Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile
50 55 60

Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg
65 70 75 80

Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser
85 90 95

Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His
100 105 110

His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro
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Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val
130 135 140

<210> 12

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PCR Primer

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<210> 13
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Combined DNA/RNA Molecule:PCR
 Primer

 <400> 13
 cuacuacuac uaggagtcct ctacggtgtt ttg 33

 <210> 14
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Combined RNA/DNA Molecule: PCR
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 <400> 14
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 <210> 15
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR Primer

 <400> 15
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 <210> 16
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR Primer

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<210> 17
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 17
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<210> 18
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 18
aactgatcta gattacttct tgaaaaagac cacgtctcc 39

<210> 19
<211> 746
<212> DNA
<213> Dictyostelium discoideum

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acaaacagta atattaataa atacaa 746

<210> 20

<211> 228

<212> PRT

<213> Dictyostelium discoideum

<220>

<223> 228 uncertain of sequence

<220>

<223> Amino acid 228 uncertain of the sequence

<400> 20

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			20					25						30	

Gln	Asp	Trp	Glu	Ala	Phe	Val	Lys	Asp	Gly	Lys	Asn	Gly	Ala	Ile	Arg
		35						40					45		

Val	Ser	Val	Ala	Thr	Asn	Phe	Asp	Lys	Ala	Ala	Tyr	Val	Ile	Gly	Lys
	50					55						60			

Leu	Ser	Phe	Val	Phe	Phe	Arg	Phe	Ile	Leu	Pro	Leu	Arg	Tyr	His	Ser
65					70					75				80	

Phe	Thr	Asp	Leu	Ile	Cys	Tyr	Phe	Leu	Ile	Ala	Glu	Phe	Val	Phe	Gly
			85						90					95	

Trp	Tyr	Leu	Thr	Ile	Asn	Phe	Gln	Val	Ser	His	Val	Ala	Glu	Asp	Leu
		100						105						110	

Lys	Phe	Phe	Ala	Thr	Pro	Glu	Arg	Pro	Asp	Glu	Pro	Ser	Gln	Ile	Asn
	115						120					125			

Glu	Asp	Trp	Ala	Ile	Leu	Gln	Leu	Lys	Thr	Thr	Gln	Asp	Tyr	Gly	His
	130					135						140			

Gly	Ser	Leu	Leu	Cys	Thr	Phe	Phe	Ser	Gly	Ser	Leu	Asn	His	Gln	Val
145				150					155					160	

Val	His	His	Leu	Phe	Pro	Ser	Ile	Ala	Gln	Asp	Phe	Tyr	Pro	Gln	Leu
			165						170					175	

Val	Pro	Ile	Val	Lys	Glu	Val	Cys	Lys	Glu	His	Asn	Ile	Thr	Tyr	His
		180						185					190		

Ile	Lys	Pro	Asn	Phe	Thr	Glu	Ala	Ile	Met	Ser	His	Ile	Asn	Tyr	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195

200

205

Tyr Lys Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser
 210 215 220

Lys Asp Asp Xaa
 225

<210> 21

<211> 494

<212> DNA

<213> *Phaeodactylum tricornutum*

<400> 21

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 ttattcccca gcctgccccg acacaatctg gccaagacac acgcactggt cgaatcggtc 180
 tgcaaggagt ggggtgtcca gtaccacgaa gccgacctcg tggacgggac catggaagtc 240
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 gccatgtaat cgtcgttcgt gacgatgcaa gggttcacgc acatctacac acactcactc 360
 acacaactag tgtaactcgt atagaattcg gtgtcgacct ggacctgtt tgactggttg 420
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 gcccgcgtna aagt 494

<210> 22

<211> 102

<212> PRT

<213> *Phaeodactylum tricornutum*

<220>

<223> Amino acid 4, 6, 10, 11, 14 and 18 uncertain of
 sequence

<400> 22

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 1 5 10 15
 Glu Xaa Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys Gly Gly
 20 25 30
 Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu Pro Arg His
 35 40 45
 Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe Cys Lys Glu Trp
 50 55 60

Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp Gly Thr Met Glu Val
65 70 75 80

Leu His His Leu Gly Ser Val Ala Gly Glu Phe Val Val Asp Phe Val
85 90 95

Arg Asp Gly Pro Ala Met
100

<210> 23

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Schizochytrium
cDNA Clone

<400> 23

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atttacattt ttctgcagtt cgccgtaagt cacaccatt tgcccgtagag caaccgggag 180
gatcagctgc attggctcga gtacgcgcgg accacactgt gaacatcagc accaagtcgt 240
ggtttgtcac atgggtggatg tcgaacctca actttcagat cgagcaccac cttttcccca 300
cggcgcccca gttccgtttc aaggagatca gccgcgcgt cgaggccctc ttcaagcgcc 360
acggtctccc ttactacgac atgccctaca cgagcgccgt ctccaccacc tttgccaacc 420
tctactcgt cggccattcc gtcggcgacg ccaagcgcgga ctagcctctt ttcctagacc 480
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<210> 24

<211> 153

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Schizochytrium
cDNA Clone

<400> 24

Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys Arg
1 5 10 15

His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His Val Leu
20 25 30

Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala Val Arg Arg

35	40	45
Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly Ser Ala Ala Leu		
50	55	60
Ala Arg Val Arg Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp		
65	70	75 80
Phe Val Thr Trp Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His		
	85 90	95
Leu Phe Pro Thr Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg		
	100 105	110
Val Glu Ala Leu Phe Lys Arg His Gly Leu Pro Tyr Tyr Asp Met Pro		
	115 120	125
Tyr Thr Ser Ala Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly		
	130 135	140
His Ser Val Gly Asp Ala Lys Arg Asp		
145	150	

<210> 25

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Schizochytrium

cDNA Clone

<400> 25

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gctgatgggt cagtcttcac cctcgcgct cgctctcggc attgtcgtca gcggcatctc 180
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ttggcttgac gaccggttgt gcgagttctt ttacggcggt gggtgtggca tgagcgggtca 300
ttactggaaa aaccagcaca gcaaacacca cgcagcgcca aaccggctcg agcacgatgt 360
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<210> 26

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Schizochytrium
cDNA Clone

<400> 26

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Phe	Asp	Pro	Ser	Leu	Pro	His	Met	Thr	Tyr	Arg	Val	Val	Glu	Ile	Val
			20					25					30		
Val	Leu	Phe	Val	Leu	Ser	Phe	Trp	Leu	Met	Gly	Gln	Ser	Ser	Pro	Leu
		35					40					45			
Ala	Leu	Ala	Leu	Gly	Ile	Val	Val	Ser	Gly	Ile	Ser	Gln	Gly	Arg	Cys
	50					55					60				
Gly	Trp	Val	Met	His	Glu	Met	Gly	His	Gly	Ser	Phe	Thr	Gly	Val	Ile
65				70						75				80	
Trp	Leu	Asp	Asp	Arg	Leu	Cys	Glu	Phe	Phe	Tyr	Gly	Val	Gly	Cys	Gly
				85					90					95	
Met	Ser	Gly	His	Tyr	Trp	Lys	Asn	Gln	His	Ser	Lys	His	His	Ala	Ala
		100						105					110		
Pro	Asn	Arg	Leu	Glu	His	Asp	Val	Asp	Leu	Asn	Thr	Leu	Pro	Leu	Val
		115					120					125			
Ala	Phe	Asn	Glu	Arg	Val	Val	Arg	Lys	Val	Arg	Pro				
	130					135				140					

<210> 27

<211> 1219

<212> DNA

<213> Homo sapiens

<400> 27

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ttacatagta	aaagacttgg	actggaaatg	ggatcatatt	ggggcctatg	cgtttggcag	180
ttgcattaac	cactcaatga	ctctggctat	tcatgagatt	gccacaatg	ctgccttttg	240
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ccccaaacca	attacgtatc	tggaagttat	caataccgtg	gcacaggtca	cttttgacat	540

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tcataatgaa	catcatgatt	tcccacacat	tcctggaaaa	agtcttccac	tggtgaggaa	780
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cagcctgact	ctgtactgct	cagtttcact	cacaggaaac	ttgtgacttg	tgtattatcg	1140
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<210> 28

<211> 655

<212> DNA

<213> Homo sapiens

<400> 28

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gaaccatatt	cccattgcaca	ttgatcatga	ccggaacatg	gactgggttt	ccacccagct	180
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gtcagccttc	gccgacatca	tccactcact	aaaggagtca	gggcagctct	ggctagatgc	420
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<210> 29

<211> 304

<212> DNA

<213> Homo sapiens

<400> 29

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cccaagtggga	accaccttgt	ccacaaattc	gtcattggcc	acttaaaggg	tgctctgcc	180
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aaga						304

<210> 30

<211> 918
 <212> DNA
 <213> Homo sapiens

<400> 30

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ccaggggggct cccgggtcat cagccactac gccgggcagg atgccacgga tccctttgtg 180
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<210> 31
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<400> 31

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<210> 32

<211> 1843

<212> DNA

<213> Homo sapiens

<400> 32

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1843

<210> 33

<211> 2257

<212> DNA

<213> Homo sapiens

<400> 33

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gtccaccctt tcatagagag gcctgctttt ttacaaagct cgggtctccc tcctgcagct 1860
cggttaagta cccgaggcct ctcttaagat gtccagggcc ccaggcccgc gggcacagcc 1920
agcccaaacc ttggggcctg gaagagtctt ccaccccatc actagagtgc tctgacctg 1980
ggctttcacg ggccccatc caccgcctcc ccaacttgag cctgtgacct tgggacaaa 2040
gggggagtc ctcgtctctt gtgactcagc agaggcagtg gccacgttca gggagggggc 2100
ggctggcctg gaggtcagc ccacctcca gcttttctc aggggtgctt gaggtccaag 2160
attctggagc aatctgacct ttctccaaag gctctgttat cagctgggca gtgccagcca 2220
atccctggcc atttgcccc aggggacgtg ggccctg 2257
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<210> 34

<211> 406

<212> PRT

<213> Homo sapiens

<220>

<223> Amino acid 331, 334, 358, 375 and 382 uncertain of
sequence

<400> 34

His Ala Asp Arg Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile Lys
1 5 10 15

Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile Met Met
20 25 30

Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp Leu Asp Trp
35 40 45

Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser Cys Ile Asn His
50 55 60

Ser Met Thr Leu Ala Ile His Glu Ile Ala His Asn Ala Ala Phe Gly
65 70 75 80

Asn Cys Lys Ala Met Trp Asn Arg Trp Phe Gly Met Phe Ala Asn Leu
85 90 95

Pro Ile Gly Ile Pro Tyr Ser Ile Ser Phe Lys Arg Tyr His Met Asp
100 105 110

His His Arg Tyr Leu Gly Ala Asp Gly Val Asp Val Asp Ile Pro Thr
115 120 125

Asp Phe Glu Gly Trp Phe Phe Cys Thr Ala Phe Arg Lys Phe Ile Trp
130 135 140

Val Ile Leu Gln Pro Leu Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn
145 150 155 160

Pro Lys Pro Ile Thr Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val
165 170 175

Thr Phe Asp Ile Leu Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val
180 185 190

Tyr Met Leu Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser

195					200					205						
Gly	His	Phe	Ile	Ala	Glu	His	Tyr	Met	Phe	Leu	Lys	Gly	His	Glu	Thr	
210					215					220						
Tyr	Ser	Tyr	Tyr	Gly	Pro	Leu	Asn	Leu	Leu	Thr	Phe	Asn	Val	Gly	Tyr	
225					230					235					240	
His	Asn	Glu	His	His	Asp	Phe	Pro	Asn	Ile	Pro	Gly	Lys	Ser	Leu	Pro	
245					250					255						
Leu	Val	Arg	Lys	Ile	Ala	Ala	Glu	Tyr	Tyr	Asp	Asn	Leu	Pro	His	Tyr	
260					265					270						
Asn	Ser	Trp	Ile	Lys	Val	Leu	Tyr	Asp	Phe	Val	Met	Asp	Asp	Thr	Ile	
275					280					285						
Ser	Pro	Tyr	Ser	Arg	Met	Lys	Arg	His	Gln	Lys	Gly	Glu	Met	Val	Leu	
290					295					300						
Glu	Xaa	Ile	Ser	Leu	Val	Pro	Lys	Gly	Phe	Phe	Ser	Lys	Thr	Leu	Asp	
305					310					315					320	
Asp	Lys	Met	Glu	Phe	Leu	His	Tyr	Xaa	Thr	Xaa	Asp	Gln	Xaa	Cys	Ser	
325					330					335						
Glu	Ala	Pro	Leu	Ala	Gln	Phe	Gln	Ser	Lys	Ser	Ser	Val	Ile	Pro	Arg	
340					345					350						
Ser	Glu	Ser	Gly	Phe	Xaa	Thr	Val	Ser	Leu	Thr	Leu	Tyr	Cys	Ser	Val	
355					360					365						
Ser	Leu	Thr	Gly	Asn	Leu	Xaa	Leu	Val	Tyr	Tyr	Arg	His	Xaa	Gly	Cys	
370					375					380						
Phe	Thr	His	Val	Cys	His	Phe	Ile	Ser	Ile	Ser	Phe	Lys	Lys	Leu	Leu	
385					390					395					400	
Lys	Ser	Tyr	Phe	Ala	Arg											
405																

<210> 35

<211> 218

<212> PRT

<213> Homo sapiens

<220>

<223> Amino acid 145, 168, 174, 186, 189, 198 and 202
uncertain of the sequence

<400> 35

Tyr	Leu	Leu	Arg	Pro	Leu	Leu	Pro	His	Leu	Cys	Ala	Thr	Ile	Gly	Ala
1				5					10					15	

Glu	Ser	Phe	Leu	Gly	Leu	Phe	Phe	Ile	Val	Arg	Phe	Leu	Glu	Ser	Asn
			20					25					30		

Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	Ile	Pro	Met	His	Ile	Asp
		35					40					45			

His	Asp	Arg	Asn	Met	Asp	Trp	Val	Ser	Thr	Gln	Leu	Gln	Ala	Thr	Cys
	50					55					60				

Asn	Val	His	Lys	Ser	Ala	Phe	Asn	Asp	Trp	Phe	Ser	Gly	His	Leu	Asn
65					70					75					80

Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Tyr
				85					90					95	

His	Lys	Val	Ala	Pro	Leu	Val	Gln	Ser	Leu	Cys	Ala	Lys	His	Gly	Ile
			100					105					110		

Glu	Tyr	Gln	Ser	Lys	Pro	Leu	Leu	Ser	Ala	Phe	Ala	Asp	Ile	Ile	His
		115					120					125			

Ser	Leu	Lys	Glu	Ser	Gly	Gln	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	Gln
	130					135					140				

Xaa	Gln	Gln	Pro	Pro	Cys	Pro	Val	Trp	Lys	Lys	Arg	Arg	Lys	Thr	Leu
145					150					155					160

Glu	Pro	Arg	Gln	Arg	Gly	Ala	Xaa	Gly	Thr	Met	Pro	Leu	Xaa	Phe	Asn
				165					170					175	

Thr	Gln	Arg	Gly	Leu	Gly	Leu	Gly	Thr	Xaa	Ser	Leu	Xaa	Leu	Lys	Leu
			180					185					190		

Leu	Pro	Phe	Ile	Phe	Xaa	Pro	Gln	Phe	Xaa	Asp	Pro	Lys	Trp	Gly	Val
		195					200					205			

Asp	Thr	Glu	Val	Pro	Arg	Arg	Glu	Gly	Ala
	210					215			

<210> 36

<211> 87
<212> PRT
<213> Homo sapiens

<220>

<223> Amino acid 87 uncertain of the sequence

<400> 36

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe
1 5 10 15

Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr
20 25 30

Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His
35 40 45

Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn
50 55 60

His Arg His Phe Gln His His Ala Lys Pro Asn Leu Gly Glu Trp Gln
65 70 75 80

Pro Ile Glu Tyr Gly Lys Xaa
85

<210> 37

<211> 306

<212> PRT

<213> Homo sapiens

<220>

<223> Amino acid 252 uncertain of the sequence

<400> 37

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln Arg
1 5 10 15

Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val Tyr Asn
20 25 30

Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg Val Ile Ser
35 40 45

His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val Ala Phe His Ile
50 55 60

Asn	Lys	Gly	Leu	Val	Lys	Lys	Tyr	Met	Asn	Ser	Leu	Leu	Ile	Gly	Glu	
65					70					75					80	
Leu	Ser	Pro	Glu	Gln	Pro	Ser	Phe	Glu	Pro	Thr	Lys	Asn	Lys	Glu	Leu	
				85					90					95		
Thr	Asp	Glu	Phe	Arg	Glu	Leu	Arg	Ala	Thr	Val	Glu	Arg	Met	Gly	Leu	
			100					105					110			
Met	Lys	Ala	Asn	His	Val	Phe	Phe	Leu	Leu	Tyr	Leu	Leu	His	Ile	Leu	
		115					120						125			
Leu	Leu	Asp	Gly	Ala	Ala	Trp	Leu	Thr	Leu	Trp	Val	Phe	Gly	Thr	Ser	
		130				135					140					
Phe	Leu	Pro	Phe	Leu	Leu	Cys	Ala	Val	Leu	Leu	Ser	Ala	Val	Gln	Ala	
145					150					155					160	
Gln	Ala	Gly	Trp	Leu	Gln	His	Asp	Phe	Gly	His	Leu	Ser	Val	Phe	Ser	
				165					170						175	
Thr	Ser	Lys	Trp	Asn	His	Leu	Leu	His	His	Phe	Val	Ile	Gly	His	Leu	
				180				185						190		
Lys	Gly	Ala	Pro	Ala	Ser	Trp	Trp	Asn	His	Met	His	Phe	Gln	His	His	
		195					200					205				
Ala	Lys	Pro	Asn	Cys	Phe	Arg	Lys	Asp	Pro	Asp	Ile	Asn	Met	His	Pro	
		210				215					220					
Phe	Phe	Phe	Ala	Leu	Gly	Lys	Ile	Leu	Ser	Val	Glu	Leu	Gly	Lys	Gln	
225					230					235					240	
Lys	Lys	Lys	Tyr	Met	Pro	Tyr	Asn	His	Gln	His	Xaa	Tyr	Phe	Phe	Leu	
				245					250					255		
Ile	Gly	Pro	Pro	Ala	Leu	Leu	Pro	Leu	Tyr	Phe	Gln	Trp	Tyr	Ile	Phe	
			260					265					270			
Tyr	Phe	Val	Ile	Gln	Arg	Lys	Lys	Trp	Val	Asp	Leu	Ala	Trp	Ile	Ser	
		275					280					285				
Lys	Gln	Glu	Tyr	Asp	Glu	Ala	Gly	Leu	Pro	Leu	Ser	Thr	Ala	Asn	Ala	
		290				295					300					
Ser	Lys															
305																

<210> 38

<211> 562

<212> PRT

<213> Homo sapiens

<220>

<223> Amino acid 242, 268, 405, 438, 464, 482, 497 and
562 uncertain of the sequence

<400> 38

His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln
1 5 10 15

His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met
20 25 30

Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys
35 40 45

Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe
50 55 60

Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile
65 70 75 80

Ile Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala
85 90 95

Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly
100 105 110

Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser
115 120 125

His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met Glu Ile
130 135 140

Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr
145 150 155 160

Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu
165 170 175

Asn Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn
180 185 190

Leu His Lys Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly

195	200	205
Ile Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile		
210	215	220
Arg Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His		
225	230	235 240
Lys Xaa Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp		
245	250	255
Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu		
260	265	270
Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro		
275	280	285
Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro		
290	295	300
Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu		
305	310	315 320
Pro Val Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro		
325	330	335
Gly Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly		
340	345	350
Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala Trp		
355	360	365
Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu Gly Phe		
370	375	380
Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp		
385	390	395 400
Leu His Ser Pro Xaa Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg		
405	410	415
Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser		
420	425	430
Thr Arg Gly Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr		
435	440	445
Ala Ser Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa		

450		455		460
Ser Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro				
465		470		475 480
Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu Leu				
	485		490	495
Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly Trp Pro				
	500		505	510
Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser				
	515		520	525
Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala				
	530		535	540
Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly				
545		550		555 560

Pro Xaa

<210> 39

<211> 615

<212> PRT

<213> Homo sapiens

<220>

<223> Amino acid 295, 321, 458, 491, 517, 535, 550 and
615 uncertain of the sequence

<400> 39

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe			
1	5	10	15
Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr			
	20	25	30
Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His			
	35	40	45
Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn			
	50	55	60
His Arg His Phe Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp			
65	70	75	80

Pro Asp Val Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro
 85 90 95

Ile Glu Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln
 100 105 110

His Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr
 115 120 125

Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val
 130 135 140

Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr
 145 150 155 160

Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile
 165 170 175

Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His
 180 185 190

Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser
 195 200 205

Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp
 210 215 220

Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
 225 230 235 240

Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser Leu
 245 250 255

Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala
 260 265 270

Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu
 275 280 285

Asp Ala Tyr Leu His Lys Xaa Ser His Ser Pro Arg Asp Thr Val Gly
 290 295 300

Lys Gly Cys Arg Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe
 305 310 315 320

Xaa Gly Val Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met
 325 330 335

Leu Asp Leu Ser Pro Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro
 340 345 350
 His Ser Thr Leu Pro Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro
 355 360 365
 Ser Ala Met Ala Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly Ala
 370 375 380
 Glu Arg Trp Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser Leu Pro
 385 390 395 400
 Leu Lys Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser
 405 410 415
 Pro Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln
 420 425 430
 Met Leu Leu Gly Phe Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu
 435 440 445
 Thr Leu Pro Ala Trp Leu His Ser Pro Xaa Arg Leu Pro Leu Val His
 450 455 460
 Pro Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro
 465 470 475 480
 Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser Xaa Asp Val Gln Gly Pro
 485 490 495
 Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys Ser Pro
 500 505 510
 Pro Pro His His Xaa Ser Ala Leu Thr Leu Gly Phe His Gly Pro His
 515 520 525
 Ser Thr Ala Ser Pro Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly
 530 535 540
 Val Pro Arg Leu Leu Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly
 545 550 555 560
 Gly Ala Gly Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln
 565 570 575
 Gly Val Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys
 580 585 590

Ala Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
595 600 605

Pro Gly Asp Val Gly Pro Xaa
610 615

<210> 40

<211> 753

<212> PRT

<213> Homo sapiens

<220>

<223> Amino acid 433, 459, 596, 629, 655, 673, 688 and
753 uncertain of the sequence

<400> 40

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln Arg
1 5 10 15

Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val Tyr Asn
20 25 30

Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg Val Ile Ser
35 40 45

His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val Ala Phe His Ile
50 55 60

Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser Leu Leu Ile Gly Glu
65 70 75 80

Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro Thr Lys Asn Lys Glu Leu
85 90 95

Thr Asp Glu Phe Arg Glu Leu Arg Ala Thr Val Glu Arg Met Gly Leu
100 105 110

Met Lys Ala Asn His Val Phe Phe Leu Leu Tyr Leu Leu His Ile Leu
115 120 125

Leu Leu Asp Gly Ala Ala Trp Leu Thr Leu Trp Val Phe Gly Thr Ser
130 135 140

Phe Leu Pro Phe Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Gln
145 150 155 160

Ala Gln Ala Gly Trp Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr
 165 170 175
 Arg Lys Pro Lys Trp Asn His Leu Val His Lys Phe Val Ile Gly His
 180 185 190
 Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His
 195 200 205
 His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu
 210 215 220
 His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys
 225 230 235 240
 Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu
 245 250 255
 Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile
 260 265 270
 Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val
 275 280 285
 Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly Ile
 290 295 300
 Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His
 305 310 315 320
 Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met Glu Ile Asp
 325 330 335
 Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys
 340 345 350
 Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn
 355 360 365
 Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu
 370 375 380
 His Lys Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile
 385 390 395 400
 Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg
 405 410 415

Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys
 420 425 430

Xaa Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly
 435 440 445

Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg
 450 455 460

Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe
 465 470 475 480

Leu Leu Ser Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro Ser
 485 490 495

Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu Pro
 500 505 510

Val Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro Gly
 515 520 525

Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly Asp
 530 535 540

Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala Trp Ser
 545 550 555 560

Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu Gly Phe Ile
 565 570 575

Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu
 580 585 590

His Ser Pro Xaa Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro
 595 600 605

Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr
 610 615 620

Arg Gly Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala
 625 630 635 640

Ser Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser
 645 650 655

Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro Thr
 660 665 670

Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu Leu Xaa
675 680 685

Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly
690 695 700

Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys
705 710 715 720

Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly
725 730 735

Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro
740 745 750

Xaa

Sub
C1
cont